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RAW SEQUENCE LISTING   DATE: 11/21/2002
PATENT APPLICATION: US/09/899,645A   TIME: 10:13:03

Input Set : A:\5718-111.app
Output Set: N:\CRF4\11212002\I899645A.raw

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 3 <110> APPLICANT: Li, Chun Ping
 4         Zheng, Peizhong
 5         Nichols, Scott
 7 <120> TITLE OF INVENTION: METHODS FOR REGULATING BETA-OXIDATION IN PLANTS
 9 <130> FILE REFERENCE: 35718/235742
11 <140> CURRENT APPLICATION NUMBER: 09/899,645A
12 <141> CURRENT FILING DATE: 2001-07-05
14 <150> PRIOR APPLICATION NUMBER: 60/216,211
15 <151> PRIOR FILING DATE: 2000-07-06
17 <160> NUMBER OF SEQ ID NOS: 8
19 <170> SOFTWARE: PatentIn Ver. 2.1
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 1169
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24 <213> ORGANISM: Zea mays
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27 <221> NAME/KEY: CDS
28 <222> LOCATION: (89)..(814)
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33 ggcacgagag actgttgatt gtctaaaa atg gtg cat agt ttg cat gca att      112
34                                  Met Val His Ser Leu His Ala Ile
35                                   1               5
37 ttt ctt gtt gct gga gac aat aac ata ccg ata ata tat caa gtt cat  160
38 Phe Leu Val Ala Gly Asp Asn Asn Ile Pro Ile Ile Tyr Gln Val His
39      10              15                  20
41 cgg gca cgt gat gga tcc agc ttt gcc aca aga aaa gtg gag gca aag  208
42 Arg Ala Arg Asp Gly Ser Ser Phe Ala Thr Arg Lys Val Glu Ala Lys
43  25              30                  35                  40
45 cag aag ggc cta gtt gta ttc acc ttg att gct tct ttc cag aag gaa  256
46 Gln Lys Gly Leu Val Val Phe Thr Leu Ile Ala Ser Phe Gln Lys Glu
47              45                  50                  55
49 gaa gtg ggt ttt gag cat cag gct gca atc atg cct gat gtt cct ccg  304
50 Glu Val Gly Phe Glu His Gln Ala Ala Ile Met Pro Asp Val Pro Pro
51              60                  65                  70
53 cca gaa cag ctc ctt aat ctg gag gag ata cgt gaa aga cgg ctt act  352
54 Pro Glu Gln Leu Leu Asn Leu Glu Glu Ile Arg Glu Arg Arg Leu Thr
55          75              80                  85
57 gat cca cgc ttc cca tcc caa tat agg aac ttg gca gct aaa aaa aag  400
58 Asp Pro Arg Phe Pro Ser Gln Tyr Arg Asn Leu Ala Ala Lys Lys Lys
59          90              95                  100
61 ttt att cct tgg ccc ata gaa atg aga ttt tgt gaa ggt tca gcg tct  448
62 Phe Ile Pro Trp Pro Ile Glu Met Arg Phe Cys Glu Gly Ser Ala Ser
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63 105                   110                115                120
65 caa cat aaa cca agc tta aac tac tgg ttt aga gct cga ggg aaa ctc   496
66 Gln His Lys Pro Ser Leu Asn Tyr Trp Phe Arg Ala Arg Gly Lys Leu
67               125                130                135
69 tca gac gac caa gct cta cac aga tgt gtt gta gca tat gct tcg gat   544
70 Ser Asp Asp Gln Ala Leu His Arg Cys Val Val Ala Tyr Ala Ser Asp
71               140                145                150
73 cta cta ttt tct ggg gtg agc ctt aac cct cat cgg gag aag ggt ttg   592
74 Leu Leu Phe Ser Gly Val Ser Leu Asn Pro His Arg Glu Lys Gly Leu
75           155                160                165
77 aag aca tac tgc ctc agt ctt gac cat tcc atc tgg ttc cac aaa cct   640
78 Lys Thr Tyr Cys Leu Ser Leu Asp His Ser Ile Trp Phe His Lys Pro
79     170                175                180
81 gtg aag gct gac gaa tgg atg ctg tat gtg atc gag agc cca tct gcg   688
82 Val Lys Ala Asp Glu Trp Met Leu Tyr Val Ile Glu Ser Pro Ser Ala
83 185                190                195                200
85 cac ggt ggt cgc ggt ttc gtc acc gga cgc atg ttc aac agg caa gga   736
86 His Gly Gly Arg Gly Phe Val Thr Gly Arg Met Phe Asn Arg Gln Gly
87               205                210                215
89 gag ctt atc atg tcg ctg acc caa gag gca ttg att cga agg gag aag   784
90 Glu Leu Ile Met Ser Leu Thr Gln Glu Ala Leu Ile Arg Arg Glu Lys
91           220                225                230
93 ccg cga gga cca aat ccg agg ccg aag ctt tgaggcacct gacagcctct   834
94 Pro Arg Gly Pro Asn Pro Arg Pro Lys Leu
95           235                240
97 gcagtcgact gtagaggatc ccaaccgagc tttgagaggc gcaccatcct ttcttctaat 894
99 ttggtttaga tatttatgaa ttcacaaaca aaaatataga atatcaagca gtataaaaga 954
101 tctcaagtca aacctaacat ttttttttcat ttctccggat gatttctatt tgttttggtg 1014
103 tgtgtgtggt tggaggggta ttggaagcgg aagcggaggc ggaggtttg atactttagg 1074
105 ctatttcctg cagcttactt tcattatacg aacagtatat atacatattt aaacttcaaa 1134
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111 <211> LENGTH: 242
112 <212> TYPE: PRT
113 <213> ORGANISM: Zea mays
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120           20                 25                 30
122 Ala Thr Arg Lys Val Glu Ala Lys Gln Lys Gly Leu Val Val Phe Thr
123           35                 40                 45
125 Leu Ile Ala Ser Phe Gln Lys Glu Glu Val Gly Phe Glu His Gln Ala
126     50                 55                 60
128 Ala Ile Met Pro Asp Val Pro Pro Glu Gln Leu Leu Asn Leu Glu
129 65                 70                 75                 80
131 Glu Ile Arg Glu Arg Arg Leu Thr Asp Pro Arg Phe Pro Ser Gln Tyr
132           85                 90                 95
134 Arg Asn Leu Ala Ala Lys Lys Lys Phe Ile Pro Trp Pro Ile Glu Met
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137 Arg Phe Cys Glu Gly Ser Ala Ser Gln His Lys Pro Ser Leu Asn Tyr
138         115                 120                 125
140 Trp Phe Arg Ala Arg Gly Lys Leu Ser Asp Asp Gln Ala Leu His Arg
141     130                 135                 140
143 Cys Val Val Ala Tyr Ala Ser Asp Leu Leu Phe Ser Gly Val Ser Leu
144 145                 150                 155                 160
146 Asn Pro His Arg Glu Lys Gly Leu Lys Thr Tyr Cys Leu Ser Leu Asp
147                 165                 170                 175
149 His Ser Ile Trp Phe His Lys Pro Val Lys Ala Asp Glu Trp Met Leu
150                 180                 185                 190
152 Tyr Val Ile Glu Ser Pro Ser Ala His Gly Gly Arg Gly Phe Val Thr
153         195                 200                 205
155 Gly Arg Met Phe Asn Arg Gln Gly Glu Leu Ile Met Ser Leu Thr Gln
156     210                 215                 220
158 Glu Ala Leu Ile Arg Arg Glu Lys Pro Arg Gly Pro Asn Pro Arg Pro
159 225                 230                 235                 240
161 Lys Leu
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167 <211> LENGTH: 960
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171 <220> FEATURE:
172 <221> NAME/KEY: CDS
173 <222> LOCATION: (1)..(957)
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178   1           5                   10                  15
180 ggc gat ccc cct ggg gac ctc cgt agc gtc ttg gtc acg acc gtg ctc   96
181 Gly Asp Pro Pro Gly Asp Leu Arg Ser Val Leu Val Thr Thr Val Leu
182             20                  25                  30
184 aac ctc gag ccg ctg gac gag gat ctc ttc aga gga agg cat tac tgg  144
185 Asn Leu Glu Pro Leu Asp Glu Asp Leu Phe Arg Gly Arg His Tyr Trp
186         35                  40                  45
188 gta ccg gcc aag agg ctg ttt ggt ggt cag atc gtg ggc cag gcc ctg  192
189 Val Pro Ala Lys Arg Leu Phe Gly Gly Gln Ile Val Gly Gln Ala Leu
190     50                  55                  60
192 gtg gct gca gcc aag tct gtg agt gaa gac gtc cac gtg cac tcc ctg  240
193 Val Ala Ala Ala Lys Ser Val Ser Glu Asp Val His Val His Ser Leu
194 65          .       70                  75                  80
196 cac tgc tac ttt gtt cgg gca ggg gac ccg aag ctg cca gta ctg tac  288
197 His Cys Tyr Phe Val Arg Ala Gly Asp Pro Lys Leu Pro Val Leu Tyr
198                 85                  90                  95
200 caa gtg gag cgg aca cga aca ggg tcg agc ttc tcg gtg cgc tct gtg  336
201 Gln Val Glu Arg Thr Arg Thr Gly Ser Ser Phe Ser Val Arg Ser Val
202             100                 105                 110
204 aag gcc gtg caa cat ggg aag ccc atc ttc atc tgc cag gcc tcc ttc  384
205 Lys Ala Val Gln His Gly Lys Pro Ile Phe Ile Cys Gln Ala Ser Phe
```

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206         115                        120                        125
208 cag cag gcc cag ccc agc ccc atg cag cac cag ttc tcc atg ccc act    432
209 Gln Gln Ala Gln Pro Ser Pro Met Gln His Gln Phe Ser Met Pro Thr
210         130                        135                        140
212 gtg cca cca cca gaa gag ctg ctt gac tgt gag acc ctc att gac cag    480
213 Val Pro Pro Pro Glu Glu Leu Leu Asp Cys Glu Thr Leu Ile Asp Gln
214 145                        150                        155                        160
216 tat tta agg gac cct aac ctc caa aag agg tac cca ttg gcg ctc aac    528
217 Tyr Leu Arg Asp Pro Asn Leu Gln Lys Arg Tyr Pro Leu Ala Leu Asn
218                        165                        170                        175
220 cga att gct gct cag gag gtc ccc att gag atc aag cca gta aac cca    576
221 Arg Ile Ala Ala Gln Glu Val Pro Ile Glu Ile Lys Pro Val Asn Pro
222         180                        185                        190
224 tcc ccc ctg agc cag ctg cag aga atg gag ccc aaa cag atg ttc tgg    624
225 Ser Pro Leu Ser Gln Leu Gln Arg Met Glu Pro Lys Gln Met Phe Trp
226         195                        200                        205
228 gtg cga gcc cgg ggc tat att ggc gag ggc gac atg aag atg cac tgc    672
229 Val Arg Ala Arg Gly Tyr Ile Gly Glu Gly Asp Met Lys Met His Cys
230         210                        215                        220
232 tgc gtg gcc gcc tat atc tcc gac tat gcc ttc ttg ggc act gca ctg    720
233 Cys Val Ala Ala Tyr Ile Ser Asp Tyr Ala Phe Leu Gly Thr Ala Leu
234 225                        230                        235                        240
236 ctg cct cac cag tgg cag cac aag gtg cac ttc atg gtc tca ctg gac    768
237 Leu Pro His Gln Trp Gln His Lys Val His Phe Met Val Ser Leu Asp
238                        245                        250                        255
240 cat tcc atg tgg ttc cac gcc ccc ttc cga gct gac cac tgg atg ctc    816
241 His Ser Met Trp Phe His Ala Pro Phe Arg Ala Asp His Trp Met Leu
242         260                        265                        270
244 tat gaa tgc gag agc ccc tgg gcc ggt ggc tct cgg ggg ctg gtc cat    864
245 Tyr Glu Cys Glu Ser Pro Trp Ala Gly Gly Ser Arg Gly Leu Val His
246         275                        280                        285
248 ggg cgg ctg tgg cgt cag gat gga gtc cta gct gtg acc tgt gcc cag    912
249 Gly Arg Leu Trp Arg Gln Asp Gly Val Leu Ala Val Thr Cys Ala Gln
250         290                        295                        300
252 gag ggc gtg atc cga gtg aag ccc cag gtc tca gag agc aag ctg tag    960
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269 Asn Leu Glu Pro Leu Asp Glu Asp Leu Phe Arg Gly Arg His Tyr Trp
270         35                        40                        45
272 Val Pro Ala Lys Arg Leu Phe Gly Gly Gln Ile Val Gly Gln Ala Leu
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273      50                    55                    60
275 Val Ala Ala Ala Lys Ser Val Ser Glu Asp Val His Val His Ser Leu
276 65                    70                    75                    80
278 His Cys Tyr Phe Val Arg Ala Gly Asp Pro Lys Leu Pro Val Leu Tyr
279                    85                    90                    95
281 Gln Val Glu Arg Thr Arg Thr Gly Ser Ser Phe Ser Val Arg Ser Val
282                    100                   105                   110
284 Lys Ala Val Gln His Gly Lys Pro Ile Phe Ile Cys Gln Ala Ser Phe
285           115                   120                   125
287 Gln Gln Ala Gln Pro Ser Pro Met Gln His Gln Phe Ser Met Pro Thr
288       130                   135                   140
290 Val Pro Pro Pro Glu Glu Leu Leu Asp Cys Glu Thr Leu Ile Asp Gln
291 145                   150                   155                   160
293 Tyr Leu Arg Asp Pro Asn Leu Gln Lys Arg Tyr Pro Leu Ala Leu Asn
294                    165                   170                   175
296 Arg Ile Ala Ala Gln Glu Val Pro Ile Glu Ile Lys Pro Val Asn Pro
297           180                   185                   190
299 Ser Pro Leu Ser Gln Leu Gln Arg Met Glu Pro Lys Gln Met Phe Trp
300           195                   200                   205
302 Val Arg Ala Arg Gly Tyr Ile Gly Glu Gly Asp Met Lys Met His Cys
303       210                   215                   220
305 Cys Val Ala Ala Tyr Ile Ser Asp Tyr Ala Phe Leu Gly Thr Ala Leu
306 225                   230                   235                   240
308 Leu Pro His Gln Trp Gln His Lys Val His Phe Met Val Ser Leu Asp
309                    245                   250                   255
311 His Ser Met Trp Phe His Ala Pro Phe Arg Ala Asp His Trp Met Leu
312                    260                   265                   270
314 Tyr Glu Cys Glu Ser Pro Trp Ala Gly Gly Ser Arg Gly Leu Val His
315           275                   280                   285
317 Gly Arg Leu Trp Arg Gln Asp Gly Val Leu Ala Val Thr Cys Ala Gln
318       290                   295                   300
320 Glu Gly Val Ile Arg Val Lys Pro Gln Val Ser Glu Ser Lys Leu
321 305                   310                   315
325 <210> SEQ ID NO: 5
326 <211> LENGTH: 2050
327 <212> TYPE: DNA
328 <213> ORGANISM: Saccharomyces cerevisiae
330 <220> FEATURE:
331 <221> NAME/KEY: CDS
332 <222> LOCATION: (501)..(1547)
334 <400> SEQUENCE: 5
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339 acaatagcga agacaatgat gacgctagcc atcggctgaa gcgtgcggcc aggaccatta 180
341 ttccctggga ggaactaaga cccgacactc tggaatctga gctgtgaaac gggcgtcctg 240
343 cttttttcatt ctacacaggc atatgtaaca gcagtgtata ggctatgtaa atcggcccaa 300
345 tcaacaaaca agcgttgctt attggacttg ctactacccc aacaaaggag agagcctttg 360
347 attgcatcct cggaagagac ggcataaaca ccgagcctca tcctacaatg aaaaaccacg 420
349 ccagttggat ataaaccaga aaagggtttc aattcagtat ccaccatgag caagacaaga 480
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